



## SEQUENCE LISTING

<110> Honeycutt, Rhonda  
McClelland, Michael

<120> A METHOD OF IDENTIFYING TARGET ORGANISMS  
BY DETERMINING THE CHARACTERISTICS OF THEIR  
INTRONIC REGION NUCLEIC ACIDS

<130> 011399-0005-999

<140> US 10/607,559

<141> 2003-06-25

<150> US 09/645,055

<151> 2000-08-23

<150> US 60/150,977

<151> 1999-08-25

<160> 59

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 attttaccca acaattttca tcattttatc cttctaaaca aatacctact ttttctttcc 180  
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<213> *Tilletia horrida*

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cgatatagta aaaatgaaat aacgaagata caatcagcag gtaaccaacg acgctctata 180  
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aaacttggag gatctattaa aatgcgaacg gaagccaaag cttatcgata tcgtctacat 420  
aataaaaagag gtagtattac tatgatcaac tacataaacg gaaatattcg acattcatca 480  
cgacttacac aacttcaccg agtatgttaa caacttcata tacctatcat ggaaccgatt 540  
ccactaacga atgataatta ctgggtttgca ggattttttg atgcagaagg tactattacg 600  
tttagtttca agaataata tctcaacta agcatatcag tatctaataa aaacatggaa 660  
gacgttcagt ggtataaaaa tatatttgga ggctatatct attttgatag tagtcaatat 720

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aagaataaat gtaaaagtca taaatcaaac cgatttttcc ttatatcgga ttattatcaa 840
ctttcagatc taaaagcata taaaaaagag agttaatata ataatctgtg gcactatttt 900
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gtggttaactg tatgtttggt attacacaat ctactaagga tattcaagtt cttcatttta 300
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ttttcccttc taaacaagta cctacttctt cttttctaga atggtttgta ggatttactg 180
aaggagacgg cagttttggt gtaagcactc gtggttaactg tatgtttggt attacacaat 240
ctactaagga tattcaagtt cttcatttta tctttgcttt acggctccgc g 291

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<210> 43
<211> 30
<212> DNA
<213> Tilletia tritici

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<400> 43
gagatcctat tttatatcaa cacctgttct 30

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<210> 44

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<211> 51  
 <212> DNA  
 <213> *Tilletia tritici*

<220>  
 <221> misc\_feature  
 <222> 2  
 <223> n = A,T,C or G

<400> 44  
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<210> 45  
 <211> 1056  
 <212> DNA  
 <213> *Candida tropicalis*

<400> 45  
 gagatcctat tttatatcaa cacctottct gattcttcgg tcaaggttgg ccctttgtaa 60  
 tacccttatt acatacgcat tacactatat gctggaaact cctatgtaca tcgtacatag 120  
 cttacttaac tactctaggt atcagttctac tcctagcccc tagagtaaaa aggttaagag 180  
 atagtagcaa tactagcagt gatgcagcag akaaccaacg gttcatattc caagctatta 240  
 atgcctatga actcagtaga tatttcagag actacacgtg taactgtatc cccttctacg 300  
 gacccattcc atcaatgatt agctgggtcta atcgatgcta atgggtgcctt taaaatcact 360  
 cataaatcac aagtaaattg tgagataata gtgcctcaga acgaggaaag aatgttaaga 420  
 gttattcaag acaagtatgg tggttctatc aggccttagat cagggtgatcg tacccttcgt 480  
 tacagattac aagataaagc tagtgtaatc accttaatac aacatgttaa tggtaacctt 540  
 catactcctt taagattaag ccaactacat cgggtatgtc ctctacttaa tatagaggct 600  
 aacatgccta tacctttaac catattttaat ggttgattta tgggctatct tgatggtaaa 660  
 ggtaacatca gatgtagagt acctaatact tacttaagtg ctacaggtaa agctgcagta 720  
 agtcttcaag gttttgttga tgttttgggt ggtgagatag tataccgtag agccagchat 780  
 ggttcatata catggaaact atcccgctcg cctagtgtgc tgttatttat gaggtatcag 840  
 amatgacata tatcacagtc aacammgcag cggagattgg gcttaatgag aaagtctatc 900  
 acttaattta catggagaaa agtggggatt taaaargatt ttctctgtta aagacatgag 960  
 twttattcca taataaatga aaataaatgc agaagatata gtccatacgc atcctgaggk 1020  
 ttatatcctg attataccag gatttgggat agtwag 1056

<210> 46  
 <211> 968  
 <212> DNA  
 <213> *Candida tropicalis*

<400> 46  
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 agagtaaaaa ggtaagaga tagtagcaat actagcagtg atgcagcaga kaaccaacgg 180  
 ttcatattcc aagctattaa tgcctatgaa cttagtagat atttcagaga ctacacgtgt 240  
 aactgtatcc ccttctacgg acccattcca tcaatgatta gctgggtctaa tcgatgctaa 300  
 tgggtgccttt aaaatcactc ataaatcaca agtaaattgt gagataatag tgcctcagaa 360  
 cgaggaaaga atgttaagag ttattcaaga caagtatggg ggttctatca ggcttagatc 420  
 aggtgatcgt acccttcggt acagattaca agataaagct agtgtaatca ccttaataca 480  
 acatgttaat ggtaaccttc atactccttt aagattaagc caactacatc gggtagtgc 540  
 tctacttaat atagaggcta acatgcctat acctttaacc atatttaatg gttgatttat 600  
 gggctatctt gatggtaaag gtaacatcag atgtagagta cctaataatct acttaagtgc 660  
 tacaggtaaa gctgcagtaa gtcttcaagg ttttgttgat gtttttgggtg gtgagatagt 720  
 ataccgtaga gccagchatg gttcatatac atggaaacta tcccgtcgac ctagtgtgct 780  
 gttatttatg aggtatcaga matgacatat atcacagtca acammgcagc ggagattggg 840  
 cttaatgaga aagtctatca cttaatttac atggagaaaa gtggggattt aaaargattt 900  
 tctctgttaa agacatgagt wttattccat aataaatgaa aataaatgca gaagatatag 960  
 tccatacg 968

<210> 47  
 <211> 41  
 <212> DNA  
 <213> Candida tropicalis

<400> 47  
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<210> 48  
 <211> 47  
 <212> DNA  
 <213> Candida tropicalis

<400> 48  
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<210> 49  
 <211> 234  
 <212> PRT  
 <213> Candida tropicalis

<220>  
 <221> VARIANT  
 <222> 4, 193, 214, 222  
 <223> Xaa = Any Amino Acid

<400> 49  
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 Asn Ser Val Asp Ile Ser Glu Thr Thr Arg Val Thr Val Ser Pro Ser  
 20 25 30  
 Thr Asp Pro Phe His Gln Trp Leu Ala Gly Thr Ile Asp Ala Asn Gly  
 35 40 45  
 Ala Phe Lys Ile Thr His Lys Ser Gln Val Asn Cys Glu Met Met Val  
 50 55 60  
 Pro Gln Asn Glu Glu Arg Met Leu Arg Val Ile Gln Asp Lys Tyr Gly  
 65 70 75 80  
 Gly Ser Ile Arg Thr Arg Ser Gly Asp Arg Thr Thr Arg Tyr Arg Leu  
 85 90 95  
 Gln Asp Lys Ala Ser Val Ile Thr Leu Met Gln His Val Asn Gly Asn  
 100 105 110  
 Thr His Thr Pro Leu Arg Leu Ser Gln Thr His Arg Val Cys Pro Thr  
 115 120 125  
 Thr Asn Met Glu Ala Asn Met Pro Met Pro Leu Thr Met Phe Asn Gly  
 130 135 140  
 Trp Phe Met Gly Tyr Phe Asp Gly Lys Gly Asn Ile Arg Cys Arg Val  
 145 150 155 160  
 Pro Asn Ile Tyr Leu Ser Ala Thr Gly Lys Ala Ala Val Ser Thr Gln  
 165 170 175  
 Gly Phe Val Asp Val Phe Gly Gly Glu Met Val Tyr Arg Arg Ala Ser  
 180 185 190  
 Xaa Gly Ser Tyr Thr Trp Lys Thr Ser Arg Arg Pro Ser Val Thr Leu  
 195 200 205  
 Phe Met Arg Tyr Gln Xaa Trp His Met Ser Gln Ser Thr Xaa Gln Arg  
 210 215 220  
 Arg Leu Gly Leu Met Arg Lys Ser Ile Thr  
 225 230

<210> 50  
 <211> 156

<212> PRT  
<213> Tilletia horrida

<400> 50  
Met Asn Tyr Thr Val Cys Trp Lys Tyr Thr Phe Asn Val Ile Ser Thr  
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Ile Ile Met Arg Gly Ile Ile Thr Ser Met Ser Arg Tyr Ser Lys Asn  
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Glu Met Thr Lys Met Gln Ser Ala Gly Asn Gln Arg Arg Ser Met Ser  
35 40 45  
Ser Thr Val Gly Thr Thr Glu Thr Met Arg Val Thr Thr Phe Ser Thr  
50 55 60  
Thr Phe Gly Gln Trp Thr Ala Gly Val Ile Asp Gly Asp Gly Ser Thr  
65 70 75 80  
Gln Thr Ser Lys Gln Gly Tyr Thr Ser Thr Glu Ile Thr Met Gly Thr  
85 90 95  
Glu Asp Thr Pro Thr Thr Arg Tyr Ile Gln Asp Lys Thr Gly Gly Ser  
100 105 110  
Ile Lys Met Arg Thr Glu Ala Lys Ala Tyr Arg Tyr Arg Thr His Asn  
115 120 125  
Lys Arg Gly Met Ile Thr Met Ile Asn Tyr Met Asn Gly Asn Ile Arg  
130 135 140  
His Ser Ser Arg Thr Thr Gln Thr His Arg Val Cys  
145 150 155

<210> 51  
<211> 115  
<212> PRT  
<213> Tilletia horrida

<400> 51  
Met Glu Pro Ile Pro Thr Thr Asn Asp Asn Tyr Trp Phe Ala Gly Phe  
1 5 10 15  
Phe Asp Ala Glu Gly Thr Ile Thr Phe Ser Phe Lys Asn Glu Tyr Pro  
20 25 30  
Gln Thr Ser Met Arg Val Ser Asn Lys Asn Met Glu Asp Val Gln Trp  
35 40 45  
Tyr Lys Asn Met Phe Gly Gly Tyr Ile Tyr Phe Asp Ser Ser Gln Tyr  
50 55 60  
Gly His Tyr Gln Trp Ser Val Gln Arg Arg Asn Asp Val Met Arg Met  
65 70 75 80  
Arg Arg Tyr Phe Lys Asn Lys Cys Lys Ser His Lys Ser Asn Arg Phe  
85 90 95  
Phe Thr Met Ser Asp Tyr Tyr Gln Thr Ser Asp Thr Lys Ala Tyr Lys  
100 105 110  
Lys Glu Ser  
115

<210> 52  
<211> 1547  
<212> DNA  
<213> Lycoperdon pyriforme

<220>  
<221> misc\_feature  
<222> 362  
<223> n = A,T,C or G

<400> 52  
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atcgattcctt aagctgttcg agggcgctcg gaaagggttaa accgtgtaaa aactgtgaaa 120

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tgtcatttgc aaaaggattg cgattccgag gatcagttag gaaaaatcta accgatcacc 180
ctaaaagcct tcctctgccca tcgaaatatt agttgtcagc accttgtcga taaaagcact 240
aatgtgtttc atgtgaacta gatgttcaag aattcatata agttgcttga gatccaaaac 300
cagcacatta atttgttcct gttgcttgat cagcaaaaaca tcaacttctg ttgctgtcac 360
anacgtgacg atcaacgaga taaattacct ttagattaaa agtgttgatt tgtagatcg 420
aaacgaaata aagaacttcg gaaattgttt tctagtaaca gaaaccgatg agttcgtcat 480
cttgaatttg gcagtgacta atgaggatga tctgattcgt atgtgctaaa aaccaatcgt 540
ccaaaatgtc tgcgacttcc aacgaagtta acgagtaata atccattgag tttgctgcata 600
tctaaggcta aagaagatcg tgtttttcct cttcaattag attgacatga ctgtgtcgaa 660
tgatttgaat aacctccaca acaagcatta gtgagatttg accctcatat gcttaattga 720
cagttaccac gagctttgca ccttgctcat aagtttataa agctatgagt aggcaatggt 780
tggttttttc gattaagcat ggtttatacc gctcttcaag tacgaagata ggaatttcct 840
cttgtagaca atggtctcag agctcgtcgt gactttcagt ttcgtcgtg ataattattg 900
tacttaatca catgttgggt tgcccttatt tccttcacca agttacatta tagagaatgg 960
atggtccgat tgatctaate tctgttcaac actttgagat tatccgtcca cagataaaat 1020
taagatttct ggacaatctc acttattata aatatgggtga taagatcagg tataatatgt 1080
ccaacacatt agaaatctct ttttgtcgaa tcggaaacaa cgctcgtctcg tcgattatta 1140
tacgaatggg gctgtccgca ttcctacttg ttaacaagta accgctatgt tcacttttgc 1200
cagttgcaaa cgagcttggt tctggcagcc atcaaatttg atagcgatgt ctgaccaggt 1260
gaacacccac ggacttttcc acgaattaca tgcagctaa ggaatataat gtgttccgat 1320
aacacgagaa atactctaata ccaaaaatcc aaggttgctg gtttcggtcg tcatacaaat 1380
cgtgaaagcg ctcggattta gatggaccgg atgacccgat aattcgtagg tcggatgtta 1440
tcatgtaccc gggatctctc tcgattattt agatcccaaa atcccctacc caaaaaacca 1500
gtaggtcttc aaatataaaa ttaatatggt cctaaaccct atcatac 1547

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<210> 53  
 <211> 203  
 <212> PRT  
 <213> Lycoperdon pyriforme

<220>  
 <221> VARIANT  
 <222> 181  
 <223> Xaa = Any Amino Acid

<400> 53

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Gly	Asn	Arg	Cys	Ser	Pro	Leu	Arg	Met	Glu	Ala	Trp	Thr	Ser	Arg	His
			20					25					30		
Ile	Trp	Tyr	Glu	Leu	Ala	Phe	Leu	Val	Cys	Asn	Gly	Trp	Val	Ser	Lys
		35					40					45			
Tyr	Leu	Asn	Thr	Arg	Ser	Thr	Phe	Arg	Ala	Pro	Leu	Thr	Val	Asn	Ser
	50					55					60				
Tyr	Thr	Pro	Ser	Leu	Glu	Trp	Leu	Arg	Thr	Thr	Pro	Pro	Met	Ser	Leu
65					70					75				80	
Val	Ser	Cys	Val	Ser	Thr	Val	Arg	Leu	Thr	Ser	Pro	Phe	Cys	Ala	Arg
				85					90					95	
Arg	Asn	Arg	Asn	Thr	Tyr	Ala	Phe	Glu	Leu	Pro	Asn	Asn	Glu	Gln	Leu
			100					105					110		
Lys	Gln	Pro	Ser	Ala	Ser	Val	Lys	Pro	Ala	Asn	Gln	Lys	Ser	Cys	Met
		115					120					125			
Thr	Ser	Thr	Val	Gly	Val	Ile	Ser	Asp	Gly	Leu	Ser	Ser	Thr	Ala	Trp
	130				135						140				
Val	Ala	Lys	Asp	Asn	Asp	Thr	Leu	Leu	Lys	Ala	Ser	Arg	Asn	Lys	Ala
145					150					155				160	
Lys	Thr	Asp	Cys	Leu	Val	Val	Lys	Ile	Arg	Phe	Pro	Leu	Asn	Arg	Ala
			165					170						175	
Thr	Ser	Ser	Ala	Xaa	Thr	Gly	Val	Val	Phe	Asn	Tyr	Lys	Thr	Thr	Ser
			180				185						190		
Ser	Leu	Ser	Leu	Phe	Asn	Tyr	Thr	Thr	Lys	Thr					
	195						200								

<210> 5  
 <211> 225  
 <212> PRT  
 <213> Tilletia indica

<400> 54  
 Met Ser Thr Arg Gly Asn Cys Met Phe Val Ile Thr Gln Ser Thr Lys  
 1 5 10 15  
 Asp Ile Gln Val Thr His Phe Ile Gln Asp Lys Thr Gly Phe Gly Arg  
 20 25 30  
 Val Ile Lys Gln Gly His Ser Thr Ser Arg Phe Ile Val Gln Asp Asn  
 35 40 45  
 Lys Asn Thr Tyr Thr Thr Thr His Thr Phe Asn Gly Asn Thr Val Thr  
 50 55 60  
 Pro Thr Lys Met Glu Ser Phe Lys Lys Phe Met Glu Met Phe Ile Lys  
 65 70 75 80  
 Asn Ser Ser Asn Tyr Ser Ile Thr Pro Ile Ser Val Trp Arg Thr Thr  
 85 90 95  
 Pro Ser Cys Asn Asp Ala Trp Ile Ser Gly Phe Thr Asp Ala Glu Gly  
 100 105 110  
 Cys Phe Thr Cys Ser Thr Thr Gly Asn Ser Thr Ala Tyr Arg Phe Arg  
 115 120 125  
 Phe Met Thr Ser Gln Lys Asn Glu Lys Asn Lys Cys Val Thr Asp His  
 130 135 140  
 Ile Ala Phe Thr Thr Asn Gly Lys Val Arg Pro His Ser Ile Gln Gly  
 145 150 155 160  
 Val Tyr Glu Thr Thr Val Asn Gly Ile Cys Asn Asn Lys Gly Val Val  
 165 170 175  
 Gln Tyr Phe Asp Lys Tyr Lys Thr Tyr Thr Lys Lys Ala Ser Ser Tyr  
 180 185 190  
 Thr Thr Trp Lys Glu Val Ser Glu Asp Thr Lys Asp Gly Lys His Thr  
 195 200 205  
 Ser Glu Ser Thr Arg Thr Ile Met Lys Glu Lys Val Met Lys Ile Asn  
 210 215 220  
 Ser  
 225

<210> 55  
 <211> 1481  
 <212> DNA  
 <213> Aspergillus niger

<400> 55  
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 atagtacttt cataaataaa tttrattttt caaattttta tataaaattt tctaattatt 180  
 tacctaataa tactttacct tcagaaaaat tcttgacttg atttatagga ttcacagaag 240  
 gtgaggggtc atttatagta aataatagag gtgatctttg ttttgttatt acacaaaaaa 300  
 ctatagatat tgaaatatta gaatttataa aagaaacttt aggttttggg aaagtaattc 360  
 aacaatctaa attaactagt agatatgtta cacaaaacaa aaaagaaata gaaatactta 420  
 ttcatttggt taatggtaat cttatattac caagtagaaa gataaaattt gaaaatttca 480  
 ttaaaggatt taatatttga ataggtaaag gtagaataaa attagatcct gttgaattaa 540  
 aacataattt tattttacct agtttaaata atagttgatt ggcaggtttt actgatgggg 600  
 aaggctgtyt tacttgttct ataggtaaag acaaaggatt tagttttaat tttaattattg 660  
 ctcaaaaatg agaggaaaaat attgaagtat tacaacatct ttgtacttta tttaattggag 720  
 gaatagtcctc aaaacatagt gtggataatg taaatgaatt tagaatagga ggattaaaaa 780  
 attgtaaaaa tatatttccc tattttgata cttatacatt attaactaaa aaatctacta 840  
 gttatatattt atgaaaagaa atatatgaag atttggttaa aaaatatcat ttagacccaa 900  
 ttaaaagggt agagatgatt gaaaaagcta gattgataaa taaaattaat taattaaaat 960  
 attagggaag aaaagtaaaag gtttaacgtg caagttttga agctcttagg acagatgtaa 1020  
 aaggatataa gatccaaaag agcaaatatt ctataatgaa tataccttat acttagttaa 1080  
 tgtttagtta ttactacttg caactcttaa gtgtaacgta tatataattt ggtatatatt 1140

gttatactta	tcaattaata	tataattgat	aaaaggaaaa	gtagtataa	acattagcga	1200
tactagtgtt	aacggtcaat	aaattttcat	gtttaaagac	cgtcggttat	ttaagtgacc	1260
gctacagact	ggttcactgg	taggtggctg	aaatgctgct	taatgtacag	tcggttcctt	1320
ccatatttta	tatatgcaca	agcccagaat	tatataatta	ctggtacctg	gatttaataa	1380
atgaacatca	atatattgat	gagaagttaa	atttgaagga	atggattctt	cggacatccg	1440
gaagtttaca	tcttaattat	accaggattt	gggatatgta	g		1481

<210> 56  
 <211> 1393  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 56						
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caaattttta	tataaaattt	tctaattatt	tacctataaa	tactttacct	tcagaaaaat	180
tcttgacttg	atttatagga	ttcacagaag	gtgaggggtc	atttatagta	aataatagag	240
gtgatctttg	ttttgttatt	acacaaaaaa	ctatagatat	tgaaatatta	gaatttataa	300
aagaaacttt	aggttttggt	aaagtaattc	aacaatctaa	attaactagt	agatatgtta	360
cacaaaacaa	aaaagaaata	gaaatactta	ttcatttggt	taatggtaat	cttatattac	420
caagtagaaa	gataaaattt	gaaaatttca	ttaaaggatt	taatatttga	ataggtaaag	480
gtagaataaa	attagatcct	gttgaattaa	aacataattt	tattttacct	agtttaaaata	540
atagttgatt	ggcagggttt	actgatgggg	aaggctgtyt	tacttgttct	ataggtaaag	600
acaaaggatt	tagttttaat	tttaatatgg	ctcaaaaatg	agaggaaaat	attgaagtat	660
tacaacatct	ttgtacttta	tttaatggag	gaatagtcct	aaaacatagt	gtggataatg	720
taaatgaatt	tagaatagga	ggattaaaaa	attgtaaaaa	tatatttccc	tattttgata	780
cttatacatt	attaactaaa	aaatctacta	gttatatatt	atgaaaagaa	atatatgaag	840
atttggttaa	aaaatatcat	ttagacccaa	ttaaaagggt	agagatgatt	gaaaaagcta	900
gattgataaa	taaaattaat	taattaaaaa	attagggaaa	aaaagtaaa	gtttaacgtg	960
caagttttga	agctcttagg	acagatgtaa	aaggatataa	gatccaaaag	agcaaataat	1020
ctataatgaa	tataaccttat	acttagttaa	tgtttagtta	ttactacttg	caactcttaa	1080
gtgtaacgta	tatataattt	ggtatatatt	gttatactta	tcaattaata	tataattgat	1140
aaaaggaaaa	gtagtataa	acattagcga	tactagtgtt	aacggtcaat	aaattttcat	1200
gtttaaagac	cgtcggttat	ttaagtgacc	gctacagact	ggttcactgg	taggtggctg	1260
aaatgctgct	taatgtacag	tcggttcctt	ccatatttta	tatatgcaca	agcccagaat	1320
tatataatta	ctggtacctg	gatttaataa	atgaacatca	atatattgat	gagaagttaa	1380
atttgaagga	atg					1393

<210> 57  
 <211> 30  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 57				
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<210> 58  
 <211> 58  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 58					
gattcttcgg	acatccggaa	gtttacatct	taattatacc	aggatttggg atagtaag	58

<210> 59  
 <211> 316  
 <212> PRT  
 <213> *Aspergillus flavus*

<220>  
 <221> VARIANT



<222> 48, 203

<223> Xaa = Any Amino Acid

<400> 59

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			20					25					30		
Asn	Leu	Ser	Phe	Lys	Phe	Asn	Tyr	Ser	Thr	Phe	Ile	Asn	Lys	Phe	Xaa
		35					40					45			
Phe	Ser	Asn	Phe	Tyr	Ile	Lys	Phe	Ser	Asn	Tyr	Leu	Pro	Asn	Asn	Thr
	50					55					60				
Leu	Pro	Ser	Glu	Lys	Phe	Leu	Thr	Trp	Phe	Ile	Gly	Phe	Thr	Glu	Gly
65					70					75					80
Glu	Gly	Ser	Phe	Ile	Val	Asn	Asn	Arg	Gly	Asp	Leu	Cys	Phe	Val	Ile
				85					90					95	
Thr	Gln	Lys	Thr	Ile	Asp	Ile	Glu	Ile	Leu	Glu	Phe	Ile	Lys	Glu	Thr
			100					105					110		
Leu	Gly	Phe	Gly	Lys	Val	Ile	Gln	Ser	Lys	Leu	Thr	Ser	Arg	Tyr	
		115					120					125			
Val	Thr	Gln	Asn	Lys	Lys	Glu	Ile	Glu	Ile	Leu	Ile	His	Leu	Phe	Asn
		130				135					140				
Gly	Asn	Leu	Ile	Leu	Pro	Ser	Arg	Lys	Ile	Lys	Phe	Glu	Asn	Phe	Ile
145					150					155					160
Lys	Gly	Phe	Asn	Ile	Trp	Ile	Gly	Lys	Gly	Arg	Ile	Lys	Leu	Asp	Pro
				165					170					175	
Val	Glu	Leu	Lys	His	Asn	Phe	Ile	Leu	Pro	Ser	Leu	Asn	Asn	Ser	Trp
			180					185					190		
Leu	Ala	Gly	Phe	Thr	Asp	Gly	Glu	Gly	Cys	Xaa	Thr	Cys	Ser	Ile	Gly
		195					200					205			
Lys	Asp	Lys	Gly	Phe	Ser	Phe	Asn	Phe	Asn	Ile	Ala	Gln	Lys	Trp	Glu
	210					215					220				
Glu	Asn	Ile	Glu	Val	Leu	Gln	His	Leu	Cys	Thr	Leu	Phe	Asn	Gly	Gly
225					230					235					240
Ile	Val	Ser	Lys	His	Ser	Val	Asp	Asn	Val	Asn	Glu	Phe	Arg	Ile	Gly
				245					250					255	
Gly	Leu	Lys	Asn	Cys	Lys	Asn	Ile	Phe	Pro	Tyr	Phe	Asp	Thr	Tyr	Thr
			260					265					270		
Leu	Leu	Thr	Lys	Lys	Ser	Thr	Ser	Tyr	Ile	Leu	Trp	Lys	Glu	Ile	Tyr
		275					280					285			
Glu	Asp	Leu	Leu	Lys	Lys	Tyr	His	Leu	Asp	Pro	Ile	Lys	Arg	Val	Glu
	290					295					300				
Met	Ile	Glu	Lys	Ala	Arg	Leu	Ile	Asn	Lys	Ile	Asn				
305					310						315				